

Figure 1A

1 CACCCTATCC TACACTACTA GGAACCTGCA CAGTCCGCCT CGGGCAGCC AAAGCTCCTC 60
 61 TGGCCACCCT GGCTCCCAA ACCCTCCAAA ACAAAGACC AGAAAAGCAC TCTCCACCA 120
 121 GCAGCCAAAC GCCTCCTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCCAGAA 180
 181 AGGCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGACTA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTTGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCAAATCAA CCCATTATG CCCTGCAGGA GGCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 1B

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961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCTCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACCTCC 1140
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCTG TGACAGCATC 1200
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D A G L N Y G H G T G H G I G N F L C V 532

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Figure 1C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTA TAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTA AAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

Figure 1D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCTTC 3120
3121 ACCTTGTTGTG GACAGTGTCT GGTTTCCCCA TTTTACAGAC AGGAAAAGTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

Figure 2A

1 CACCCTATCC TACTACTACTA GGAACCTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TCCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGTC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGAATA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC CGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTTGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 2B

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961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCTTACA CGCTGCTCAC AGACTCTTCT 1080
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAAGTCC 1140
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCTG TGACAGCATC 1200
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCCTCC 1500
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCCGAG AGCCTTGTGG 1800
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D A G L N Y G H G T G H G I G N F L C V 532

```

Figure 2C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATTT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCGGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCCTA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAATAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCCGA CATGGAACCC ATGATTCTTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

Figure 2D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTGGAG AACAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACCTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTGG ATGCCCCCTC 3120
3121 ACCTTGTTG GACAGTGTCT GGTTCCTCCA TTTCACAGAC AGGAAACTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

Figure 3A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTG 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGGCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTTGT TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGGTGACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

 721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

 781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

Figure 3B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

1081 CC 1082

Figure 4A

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1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1      M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGTC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCAATCAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCAAC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 4B

901 TTCTTTGCCT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCAGCTC 960
 299 F F A F T N S S L N P V I Y V F V G Q L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
 319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
 339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

1081 CC 1082

Figure 5A

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1 CTGTGCATGG CATCATCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCAA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTG 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTGTCTTGG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCAATCAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGC GGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 5B

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901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082
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1081 CC 1082

Figure 6A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACT 60
1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACCTGCT CCTGAGCTCA CCCATGCTGG TGTCCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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Figure 6B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAAGTCTT GGGAGGTGTÀ CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

 1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTTGTGTÀ AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCAGGAA TGCCAAGGAG 1260
 1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320
 1321 TCCTGCCCTG CCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380
 1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440
 1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500
 1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560
 1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620
 1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATTA ATAAAGGTTA AGCCCTGAGG 1680
 1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740
 1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTÀ TATGCAGTAT 1800
 1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860
 1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920
 1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980
 1981 CCAATAACTÀ TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 6C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
3181 GAGCCCATAA ATCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

Figure 6D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCACCAAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTCACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

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Figure 7A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTCTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACA ACTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 7B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CTTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

Figure 8A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCTT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 8B

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961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCTCTCTG 1020
251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCTGC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGCGGAC 1200
311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCTCCA ATGTGCTCTC CTAGGCCACA 1440
391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

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Figure 9A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTGAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TATGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTA CTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 9B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGCGGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCGTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGACC TTGACCTGC CTCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

Figure 10A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGACTCAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCTTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACCTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACAACCTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTTCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TCTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 10B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTCCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

 1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

 1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

 1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

 1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

 1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

 1321 GACGGCCCCA AGGCCACACC CTCATCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

 1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

 1441 GGGCCTTTGG CAGGTGCAGC CCCCACTGCC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

 1501 TCCCTTCATC TGGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

 1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

 1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

 1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

 1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

Figure 11A

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1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60

61 ATGCCTCCA GGCTGACCTT GCTGACCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
41 G E G K V A T T V I S K M L F V E P I L 60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTGAGCA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCTTGCTCG GGGCTGGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCTGT ACAGCAGCAG CCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCTCCTC AATGCTATCT ACCTGAGTGC CAAGTGGGAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

```

Figure 11B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTTCATGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 12A

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1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
41 G E G K V A T T V I S K M L F V E P I L 60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTTCAGCA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCTGT ACAGCAGCAG CCCAGAGTCT CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

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Figure 12B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACCTTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTC AAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGTCA GGATATGCTC TCAATCATGG AGAAATGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 13A

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1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCACAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGCTGA ACCCATCCTG 240
41 G E G K V A T T V I S K M L F A E P I L 60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
141 V L G D A L V D F S L K L Y H A F S A M 160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTGAGCA TCGCCAGCCT CCTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

```

Figure 13B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCAATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AACCTGACA GACCAT 1826

Figure 14A

```

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60

61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
1 M A S R L T L L T L L L L L L A G D R A 20

121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
21 S S N P N A T S S S S Q D P E S L Q D R 40

181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCTCG 240
41 G E G K V A T T V I S K M L F V E P I L 60

241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
61 E V S S L P T T N S T T N S A T K I T A 80

301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
81 N T T D E P T T Q P T T E P T T Q P T I 100

361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
101 Q P T Q P T T Q L P T D S P T Q P T T G 120

421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
121 S F C P G P V T L C S D L E S H S T E A 140

481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGGAATG 540
141 V L G D A L V D F S L K L Y H A F S G M 160

541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTGAGCA TCGCCAGCCT CTTACCCAG 600
161 K K V E T N M A F S P F S I A S L L T Q 180

601 GTCCTGCTCG GGGCTGGGCA GAACACCAA ACAAACCTGG AGAGCATCCT CTCTTACCCC 660
181 V L L G A G Q N T K T N L E S I L S Y P 200

661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
201 K D F T C V H Q A L K G F T T K G V T S 220

721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
221 V S Q I F H S P D L A I R D T F V N A S 240

781 CGGACCCGTG ACAGCAGCAG CCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
241 R T L Y S S S P R V L S N N S D A N L E 260

841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
261 L I N T W V A K N T N N K I S R L L D S 280

901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGGAAG 960
281 L P S D T R L V L L N A I Y L S A K W K 300

```

Figure 14B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCTTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTTCATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTTCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCGTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F V 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 15A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGTTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F V E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGCAATG 540
 141 V L G D A L V D F S L K L Y H A F S A M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTTCAGCA TCGCCAGCCT CCTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAACCTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 15B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACTTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGCCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAGTACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCATG 1500
 461 A I S V A R T L L V F E V Q Q P F L F M 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGAAGTGGCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 16

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1 TCCTCCACCT GCTGGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTG CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180
29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTGTTG ACGACGAAAA CACAGCCCAG 300
69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCACAC CTTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCGA GGAACCCGAA 480
129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAGCC 600
169 P D D L Q C V D L K I L P N D E C K K A 188

601 CACGTCCAGA AGGTGACAGA CTTGATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAGG GGGCCCCTGG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S Y V K W I E D T I A E N S * 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

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Figure 17

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1 TCCTCCACCT GCTGGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
1 M W F L V L C L 8

61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
9 A L S L G G T G A A P P I Q S R I V G G 28

121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATT T CAGCACTTTC 180
29 W E C E Q H S Q P W Q A A L Y H F S T F 48

181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
49 Q C G G I L V H R Q W V L T A A H C I S 68

241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
69 D N Y Q L W L G R H N L F D D E N T A Q 88

301 TTTGTTCATG TCAGTGAGAG CTTCCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
89 F V H V S E S F P H P G F N M S L L E N 108

361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
109 H T R Q A D E D Y S H D L M L L R L T E 128

421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCACCGA GGAACCCGAA 480
129 P A D T I T D A V K V V E L P T E E P E 148

481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
149 V G S T C L A S G W G S I E P E N F S F 168

541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CGAAAAAGCC 600
169 P D D L Q C V D L K I L P N D E C E K A 188

601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
189 H V Q K V T D F M L C V G H L E G G K D 208

661 ACCTGTGTGG GTGATTCAGG GGGCCCCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
209 T C V G D S G G P L M C D G V L Q G V T 228

721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
229 S W G Y V P C G T P N K P S V A V R V L 248

781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
249 S Y V K W I E D T I A E N S * 262

841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

```

Figure 18

1 TCCTCCACCT GCTGGCCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTC AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATT T CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAAA CACAGCCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTCATG TCAGTGAGAG CTTCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCCCACCA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T Q E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C K K A 188
 601 CACGTCCAGA AGGTGACAGA CTTTCATGCTG TGTGTGGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTCAGG GGGCCCCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCT AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAAATCA AATGTGCATC C 871

Figure 19

BRB1_MOUSE MASQ.ASLKLPNSQSQAPPNITSCEGAPEAWDLLCRVLPGFVITVCFFGLLGNLLVLS
 BRB1_RAT MASE.VLLELPNSNRSLOAPANITSCESALEDWDLRYRVLPGFVITICFFGLLGNLLVLS
 BRB1_HUMAN MASSWPPLELQSSNQSQLFPQNATACDPAEAWDLLHRVLPFTFIIISICFFGLLGNLFVLL
 BRB1_RABIT MASQ.CPLELPNSNQSQLAPPNATSCSGAPDAWDLHRLPFTFIIAIFTLGLLGNSFVLS

BRB1_MOUSE FFLLPWRRW...QRRRRLTIAEIYLANLAASDLVFLGLPFWAENVGNRFNWPFGS DL
 BRB1_RAT FFLLPWRQWWQQRQRQRLTIAEIYLANLAASDLVFLGLPFWAENVGNRFNWPFGTDL
 BRB1_HUMAN VFLLP.....RRQLNVAEIYLANLAASDLVFLGLPFWAENVNQNFWPFGALL
 BRB1_RABIT VFLLA.....RRRLSVAEIYLANLAASDLVFLGLPFWAENVNQNFDWPFGAAL

BRB1_MOUSE CRVVS GVIKANLFISIFLVVAISQDRYRLVYPMTSWGNRRRRRQAQVTCLLI WVAGGLLS
 BRB1_RAT CRVVS GVIKANLFVSIFLVVAISQDRYRLVYPMTSWGYRRRRRQAQATCLLI WVAGGLLS
 BRB1_HUMAN CRVINGVIKANLFISIFLVVAISQDRYRLVHVPMSGRQRRRQAQVTCVLIWVVGGLLS
 BRB1_RABIT CRVINGVIKANLFISIFLVVAISQDRYSVLVHPMASRRGRRRRQAQATCALI WAGGLLS

BRB1_MOUSE TPTFLLRSVKVVPDLNITSACILLFPHEAWHFVRMVELNVLGFLPLAAILFFNYHILASL
 BRB1_RAT IPTFLLRSVKVVPDLNVSACILLFPHEAWHFARMVELNVLGFLLPVTAIFFNYHILASL
 BRB1_HUMAN IPTFLLRSIQAVPDLNITSACILLFPHEAWHFARIVELNVLGFLPLAAILFFNYHILASL
 BRB1_RABIT TPTFVLRSVRAVPELNV SACILLFPHEAWHWRMVELNVLGFLPLAAILFFNCHILASL

*

BRB1_MOUSE RGQKEASRTRCGGPKDSKTMGLILTLVASFLVCWAPYHFFAFLEFLVQVRVIQDCFWKEL
 BRB1_RAT RGQKEASRTRCGGPKGSKTTGLILTLVASFLVCWCPYHFFAFLEFLVQVRVIQDCSWKEI
 BRB1_HUMAN RTREEVSRTVRGPKDSKTTALILTLVVAFLVCWAPYHFFAFLEFLFQVQAVRGCFWEDF
 BRB1_RABIT RRRGERVPSRCGGPRDSKSTALILTLVASFLVCWAPYHFFAFLECLWQVHAIGGCFWEEF

*

BRB1_MOUSE TDLGLQLANFFAFVNSCLNPLIYVFAG LEKTRVLGTL~~~~~
 BRB1_RAT TDLGLQLANFFAFVNSCLNPLIYVFAG LLKTRVLGTL~~~~~
 BRB1_HUMAN IDLGLQLANFFAFVNSCLNPVIYVFVG LFRTKWELYKQCTPKSLAPVSSSHRKEIFQL
 BRB1_RABIT TDLGLQLSNFSAFVNSCLNPVIYVFVG LFRTKWELCQQCSPRSLAPVSSSRKEMLWG

BRB1_MOUSE ~~~~
 BRB1_RAT ~~~~
 BRB1_HUMAN FWRN
 BRB1_RABIT FWRN

Figure 20

BRB2_MOUSE ~~~~~MPCSWKLLGFISVHE.PMPTAASFGIEMFNITIQVLGSALNGTISKDN.CPDTEW
 BRB2_RAT MDTRSSLCP.KTQAVVAVFW.GPGCHLSTCIEMFNITIQALGSAHNGTFSEVN.CPDTEW
 BRB2_RABIT ~~~~~MLNITSQVLAPALNGSVSOSGCPNTEW
 BRB2_CAVPO ~~~~~MFNITSQV..SALNATIAOGNSCLDAEW
 BRB2_HUMAN ~~~~~MFSPWKISMFLSVREDSVPTTASFADMLNVTLO..GPTLNCTFAQ.SKCPQVEW

BRB2_MOUSE WSWLNAIQAPFLWVLFLLAALENIFVLSVFFLHKNSCTVAEITYLGNLAAADLILACGLPF
 BRB2_RAT WSWLNAIQAPFLWVLFLLAALENIFVLSVFFLHKNSCTVAEITYLGNLAAADLILACGLPF
 BRB2_RABIT SGWLNVIQAPFLWVLFVLATLENIFVLSVFFLHKSSCTVAEITYLGNLAAADLILACGLPF
 BRB2_CAVPO WSWLNITQAPFLWVLFVLAVLENIFVLSVFFLHKSSCTVAEITYLGNLAAADLILACGLPF
 BRB2_HUMAN LGWLNITQAPFLWVLFVLATLENIFVLSVFFLHKSSCTVAEITYLGNLAAADLILACGLPF

BRB2_MOUSE WAITIANNFDWVFGEVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMSMGRMRGVR
 BRB2_RAT WAITIANNFDWVFGEVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMSMGRMRGVR
 BRB2_RABIT WAITIANHFDWLFGEALCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMSMGRMRVR
 BRB2_CAVPO WAITIANNFDWLFGEVLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMSMGRMRGVR
 BRB2_HUMAN WAITISNNFDWLFGETLCRVVNTMIYMNLYSSICFLMLVSIIDRYLALVKTMSMGRMRGVR

BRB2_MOUSE WAKLYSLVIWGCTLLLSPPMLVFRTMKDYRESEEGHNVTACVIVYPSRSWEVFTNVLLNLVG
 BRB2_RAT WAKLYSLVIWCTLLLSPPMLVFRTMKDYRESEEGHNVTACVIVYPSRSWEVFTNVLLNLVG
 BRB2_RABIT WAKLYSLVIWGCTLLLSPPMLVFRTMKDYRDEGYNTACIIDYPSRSWEVFTNVLLNLVG
 BRB2_CAVPO WAKLYSLVIWGCTLLLSPPMLVFRTMKDYRDEGHNVTAIIYPSLIWQVFTNVLLNLVG
 BRB2_HUMAN WAKLYSLVIWGCTLLLSPPMLVFRTMKDYSEEGHNVTACVISYPSLIWEVFTNVLLNLVG

BRB2_MOUSE FLLPLSVITFCTVRIQVLRNNEMKKFKEVQTERKATVLVLAVLGLFVLCWVFPQISTFL
 BRB2_RAT FLLPLSVITFCTVRIMQVLRNNEMKKFKEVQTEKKATVLVLAVLGLFVLCWVFPQISTFL
 BRB2_RABIT FLLPLSVITFCTVQIQVLRNNEMQKFKEIQTERRATVLVLAVLLLFVLCWLPFQISTFL
 BRB2_CAVPO FLLPLSVITFCTVQIMQVLRNNEMQKFKEIQTERRATVLVLAVLLLFVLCWLPFQISTFL
 BRB2_HUMAN FLLPLSVITFCTVQIMQVLRNNEMQKFKEIQTERRATVLVLAVLLLFVLCWLPFQISTFL

BRB2_MOUSE DTLRLGLVLSGCWDEHADVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYRVLCQ
 BRB2_RAT DTLRLGLVLSGCWNERADVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYQATCR
 BRB2_RABIT DTLRLGLVLSGCWDEHVIDVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYRAACP
 BRB2_CAVPO DTLRLGLVLSGCWDEHVIDVITQISSYVAYSNSCLNPLVYVIVGKRFRKKSREVVYHGLCR
 BRB2_HUMAN DTLRLGLVLSGCQDERVIDVITQIASFMAYSNSCLNPLVYVIVGKRFRKKSREVVYQGVCCQ

*

BRB2_MOUSE K GCMGEPVQMENSMTLRTSISVERQIHKLQDWAGKKQ~~~~~
 BRB2_RAT K GCMGESVQMENSMTLRTSISVDRQIHKLQDWAGNKO~~~~~
 BRB2_RABIT KAGCVLEPVQAESSMTLRTSISVERQIHKLPEWTRSSQ~~~~~
 BRB2_CAVPO S GCVSEPAQSENSMTLRTSISVDRQIHKLQDWARSSEGTTPPGLL
 BRB2_HUMAN K GCRSEPTQMENSMTLRTSISVERQIHKLQDWAGSRQ~~~~~

Figure 21A

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1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1      M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCNA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAANGG GGTCATCAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCAAC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GNCAGGCCCG GGTCACCTGC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCNTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I X L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGANGAGGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCONGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R V X G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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1081 CC 1082

[illegible]

Figure 22A

1 AATTCAGAGC CACCGCGGGC AGGCGGGCAG TGCATCCAGA AGCGTTTATA TTCTGAGCGC 60
 61 CAGTTCAGCT TTCAAAAAGA GTGCTGCCCA TAAAAAGCCT TCCACCCTCC TGTCTGCTTT 120
 121 AGAAGGACCC TGAGCCCCAG GCGCCAGCCA CAGGACTCTG CTGCAGAGGG GGGTTGTGTA 180
 181 CAGATAGTAG GCTTTACGCC TAGCTTCGAA ATGGATAACG TCCTCCCGGT GGA CTCTAGAC 240
 1 M D N V L P V D S D 10
 241 CTCTCCCCAA ACATCTCCAC TAACACCTCG GAACCCAATC AGTTCGTGCA ACCAGCCTGG 300
 11 L S P N I S T N T S E P N Q F V Q P A W 30
 301 CAAATTGTCC TTTGGGCAGC TGCCTACACG GTCATTGTGG TGACCTCTGT GGTGGGCAAC 360
 31 Q I V L W A A A Y T V I V V T S V V G N 50
 361 GTGGTAGTGA TGTGGATCAT CTTAGCCCAC AAAAGAATGA GGACAGTGAC GAACTATTTT 420
 51 V V V M W I I L A H K R M R T V T N Y F 70
 421 CTGGTGAACC TGGCCTTCGC GGAGGCCTCC ATGGCTGCAT TCAATACAGT GGTGAACTTC 480
 71 L V N L A F A E A S M A A F N T V V N F 90
 481 ACCTATGCTG TCCACAACGA ATGGTACTAC GGCCTGTTCT ACTGCAAGTT CCACA ACTTC 540
 91 T Y A V H N E W Y Y G L F Y C K F H N F 110
 541 TTNCCCATCG CCGCTGTCTT CGCCAGTATC TACTCCATGA CGGCTGTGGC CTTTGATAGG 600
 111 F P I A A V F A S I Y S M T A V A F D R 130
 601 TACATGGCCA TCATACATCC CCTCCAGCCC CGGCTGTCAG CCACAGCCAC CAAAGTGGTC 660
 131 Y M A I I H P L Q P R L S A T A T K V V 150
 661 ATCTGTGTCA TTTGGGTCCT GGCTCTCCTG CTGGCCTTCC CCCAGGGCTA CTACTCAACC 720
 151 I C V I W V L A L L L A F P Q G Y Y S T 170
 721 ACAGAGACCA TGCCAGCAG AGTCGTGTGC ATGATCGAAT GGCCAGAGCA TCCGAACAAG 780
 171 T E T M P S R V V C M I E W P E H P N K 190
 781 ATTTATGAGA AAGTGTACCA CATCTGTGTG ACTGTGCTGA TCTACTTCCT CCCCTGCTG 840
 191 I Y E K V Y H I C V T V L I Y F L P L L 210
 841 GTGATTGGCT ATGCATACAC CGTAGTGGGA ATCACACTAT GGGCCAGTGA GATCCCCGGG 900
 211 V I G Y A Y T V V G I T L W A S E I P G 230
 901 GACTCCTCTG ACCGCTACCA CGAGCAAGTC TCTGCCAAGC GCAAGGTGGT CAAAATGATG 960
 231 D S S D R Y H E Q V S A K R K V V K M M 250

Figure 22B

961 ATTGTCGTGG TGTGCACCTT CGCCATCTGC TGGCTGCCCT TCCACATCTT CTTCTCCTG 1020
 251 I V V V C T F A I C W L P F H I F F L L 270

1021 CCCTACATCA ACCCAGATCT CTACCTGAAG AAGTTTATCC AGCAGGTCTA CCTGGCCATC 1080
 271 P Y I N P D L Y L K K F I Q Q V Y L A I 290

1081 ATGTGGCTGG CCATGAGCTC CACCATGTAC AACCCCATCA TCTACTGCTG CCTCAATGAC 1140
 291 M W L A M S S T M Y N P I I Y C C L N D 310

1141 AGGTTCCGTC TGGGCTTCAA GCATGCCTTC CGGTGCTGCC CCTTCATCAG CGCCGGCGAC 1200
 311 R F R L G F K H A F R C C P F I S A G D 330

1201 TATGAGGGGC TGGAAATGAA ATCCACCCGG TATCTCCAGA CCCAGGGCAG TGTGTACAAA 1260
 331 Y E G L E M K S T R Y L Q T Q G S V Y K 350

1261 GTCAGCCGCC TGGAGACCAC CATCTCCACA GTGGTGGGGG CCCACGAGGA GGAGCCAGAG 1320
 351 V S R L E T T I S T V V G A H E E E P E 370

1321 GACGGCCCCA AGGCCACACC CTCNTCCCTG GACCTGACCT CCAACTGCTC TTCACGAAGT 1380
 371 D G P K A T P S S L D L T S N C S S R S 390

1381 GACTCCAAGA CCATGACAGA GAGCTTCAGC TTCTCTCCA ATGTGCTCTC CTAGGCCACA 1440
 391 D S K T M T E S F S F S S N V L S * 407

1441 GGGCCTTTGG CAGGTGCAGC CCCCCTGCTC TTTGACCTGC CTCCCTTCAT GCATGGAAAT 1500

1501 TCCCTTCATC TGAACCATC AGAAACACCC TCACACTGGG ACTTGCAAAA AGGGTCAGTA 1560

1561 TGGGTTAGGG AAAACATTCC ATCCTTGAGT CAAAAAATCT CAATTCTTCC CTATCTTTGC 1620

1621 CACCCTCATG CTGTGTGACT CAAACCAAAT CACTGAACTT TGCTGAGCCT GTAAAATAAA 1680

1681 AGGTCGGACC AGCTTTTCCT CAAGAGCCCA ATGCATTCCA TTTCTGGAAG TGACTTTGGC 1740

1741 TGCATGCGAG TGCTCATTTT AGGATG 1766

Figure 23A

1 AGTCTGCACT GGAGCTGCCT GGTGACCAGA AGTTTGGAGT CCGCTGACGT CGCCGCCAG 60
 61 ATGGCCTCCA GGCTGACCCT GCTGACCCTC CTGCTGCTGC TGCTGGCTGG GGATAGAGCC 120
 1 M A S R L T L L T L L L L L A G D R A 20
 121 TCCTCAAATC CAAATGCTAC CAGCTCCAGC TCCCAGGATC CAGAGAGTTT GCAAGACAGA 180
 21 S S N P N A T S S S S Q D P E S L Q D R 40
 181 GGCGAAGGGA AGGTCGCAAC AACAGTTATC TCCAAGATGC TATTCGNTGA ACCCATCCTG 240
 41 G E G K V A T T V I S K M L F X E P I L 60
 241 GAGGTTTCCA GCTTGCCGAC AACCAACTCA ACAACCAATT CAGCCACCAA AATAACAGCT 300
 61 E V S S L P T T N S T T N S A T K I T A 80
 301 AATACCACTG ATGAACCCAC CACACAACCC ACCACAGAGC CCACCACCCA ACCCACCATC 360
 81 N T T D E P T T Q P T T E P T T Q P T I 100
 361 CAACCCACCC AACCAACTAC CCAGCTCCCA ACAGATTCTC CTACCCAGCC CACTACTGGG 420
 101 Q P T Q P T T Q L P T D S P T Q P T T G 120
 421 TCCTTCTGCC CAGGACCTGT TACTCTCTGC TCTGACTTGG AGAGTCATTC AACAGAGGCC 480
 121 S F C P G P V T L C S D L E S H S T E A 140
 481 GTGTGGGGG ATGCTTTGGT AGATTTCTCC CTGAAGCTCT ACCACGCCTT CTCAGNAATG 540
 141 V L G D A L V D F S L K L Y H A F S X M 160
 541 AAGAAGGTGG AGACCAACAT GGCCTTTTCC CCATTTCAGCA TCGCCAGCCT CCTTACCCAG 600
 161 K K V E T N M A F S P F S I A S L L T Q 180
 601 GTCCTGCTCG GGGCTGGGCA GAACACCAAA ACAAACTGG AGAGCATCCT CTCTTACCCC 660
 181 V L L G A G Q N T K T N L E S I L S Y P 200
 661 AAGGACTTCA CCTGTGTCCA CCAGGCCCTG AAGGGCTTCA CGACCAAAGG TGTCACCTCA 720
 201 K D F T C V H Q A L K G F T T K G V T S 220
 721 GTCTCTCAGA TCTTCCACAG CCCAGACCTG GCCATAAGGG ACACCTTTGT GAATGCCTCT 780
 221 V S Q I F H S P D L A I R D T F V N A S 240
 781 CGGACCCTGT ACAGCAGCAG CCCCAGAGTC CTAAGCAACA ACAGTGACGC CAACTTGGAG 840
 241 R T L Y S S S P R V L S N N S D A N L E 260
 841 CTCATCAACA CCTGGGTGGC CAAGAACACC AACAAACAAGA TCAGCCGGCT GCTAGACAGT 900
 261 L I N T W V A K N T N N K I S R L L D S 280
 901 CTGCCCTCCG ATACCCGCCT TGTCTCTCTC AATGCTATCT ACCTGAGTGC CAAGTGAAG 960
 281 L P S D T R L V L L N A I Y L S A K W K 300

Figure 23B

961 ACAACATTTG ATCCCAAGAA AACCAGAATG GAACCCCTTC ACTTCAAAAA CTCAGTTATA 1020
 301 T T F D P K K T R M E P F H F K N S V I 320

1021 AAAGTGCCCA TGATGAATAG CAAGAAGTAC CCTGTGGCCC ATTCATTGA CCAAACCTTG 1080
 321 K V P M M N S K K Y P V A H F I D Q T L 340

1081 AAAGCCAAGG TGGGGCAGCT GCAGCTCTCC CACAATCTGA GTTTGGTGAT CCTGGTACCC 1140
 341 K A K V G Q L Q L S H N L S L V I L V P 360

1141 CAGAACCTGA AACATCGTCT TGAAGACATG GAACAGGCTC TCAGCCCTTC TGTTTTCAAG 1200
 361 Q N L K H R L E D M E Q A L S P S V F K 380

1201 GCCATCATGG AGAAACTGGA GATGTCCAAG TTCCAGCCCA CTCTCCTAAC ACTACCCCGC 1260
 381 A I M E K L E M S K F Q P T L L T L P R 400

1261 ATCAAAGTGA CGACCAGNCA GGATATGCTC TCAATCATGG AGAAATTGGA ATTCTTCGAT 1320
 401 I K V T T S Q D M L S I M E K L E F F D 420

1321 TTTTCTTATG ACCTTAACCT GTGTGGGCTG ACAGAGGACC CAGATCTTCA GGTTCCTGCG 1380
 421 F S Y D L N L C G L T E D P D L Q V S A 440

1381 ATGCAGCACC AGACAGTGCT GGAAC TGACA GAGACTGGGG TGGAGGCGGC TGCAGCCTCC 1440
 441 M Q H Q T V L E L T E T G V E A A A A S 460

1441 GCCATCTCTG TGGCCCGCAC CCTGCTGGTC TTTGAAGTGC AGCAGCCCTT CCTCTTCNTG 1500
 461 A I S V A R T L L V F E V Q Q P F L F X 480

1501 CTCTGGGACC AGCAGCACAA GTTCCCTGTC TTCATGGGGC GAGTATATGA CCCCAGGGCC 1560
 481 L W D Q Q H K F P V F M G R V Y D P R A 500

1561 TGAGACCTGC AGGATCAGGT TAGGGCGAGC GCTACCTCTC CAGCCTCAGC TCTCAGTTGC 1620

1621 AGCCCTGCTG CTGCCTGCCT GGA CTTGCCC CTGCCACCTC CTGCCTCAGG TGTCCGCTAT 1680

1681 CCACCAAAAG GGCTCCTGAG GGTCTGGGCA AGGGACCTGC TTCTATTAGC CCTTCTCCAT 1740

1741 GGCCCTGCCA TGCTCTCCAA ACCACTTTTT GCAGCTTTCT CTAGTTCAAG TTCACCAGAC 1800

1801 TCTATAAATA AAACCTGACA GACCAT 1826

Figure 24

1 TCCTCCACCT GCTGGCCCCT GGACACCTCT GTCACCATGT GGTTCCTGGT TCTGTGCCTC 60
 1 M W F L V L C L 8
 61 GCCCTGTCCC TGGGGGGGAC TGGTGCTGCG CCCCCGATTG AGTCCCGGAT TGTGGGAGGC 120
 9 A L S L G G T G A A P P I Q S R I V G G 28
 121 TGGGAGTGTG AGCAGCATTC CCAGCCCTGG CAGGCGGCTC TGTACCATTG CAGCACTTTC 180
 29 W E C E Q H S Q P W Q A A L Y H F S T F 48
 181 CAGTGTGGGG GCATCCTGGT GCACCGCCAG TGGGTGCTCA CAGCTGCTCA TTGCATCAGC 240
 49 Q C G G I L V H R Q W V L T A A H C I S 68
 241 GACAATTACC AGCTCTGGCT GGGTCGCCAC AACTTGTTTG ACGACGAAA CACAGCCCAG 300
 69 D N Y Q L W L G R H N L F D D E N T A Q 88
 301 TTTGTTCATG TCAGTGAGAG CTTCCACAC CCTGGCTTCA ACATGAGCCT CCTGGAGAAC 360
 89 F V H V S E S F P H P G F N M S L L E N 108
 361 CACACCCGCC AAGCAGACGA GGACTACAGC CACGACCTCA TGCTGCTCCG CCTGACAGAG 420
 109 H T R Q A D E D Y S H D L M L L R L T E 128
 421 CCTGCTGATA CCATCACAGA TGCTGTGAAG GTCGTGGAGT TGCCACCA GGAACCCGAA 480
 129 P A D T I T D A V K V V E L P T X E P E 148
 481 GTGGGGAGCA CCTGTTTGGC TTCCGGCTGG GGCAGCATCG AACCAGAGAA TTTCTCATTT 540
 149 V G S T C L A S G W G S I E P E N F S F 168
 541 CCAGATGATC TCCAGTGTGT GGACCTCAAA ATCCTGCCTA ATGATGAGTG CNAAAAAGCC 600
 169 P D D L Q C V D L K I L P N D E C X K A 188
 601 CACGTCCAGA AGGTGACAGA CTTCATGCTG TGTGTCGGAC ACCTGGAAGG TGGCAAAGAC 660
 189 H V Q K V T D F M L C V G H L E G G K D 208
 661 ACCTGTGTGG GTGATTCAGG GGGCCCCTG ATGTGTGATG GTGTGCTCCA AGGTGTCACA 720
 209 T C V G D S G G P L M C D G V L Q G V T 228
 721 TCATGGGGCT ACGTCCCTTG TGGCACCCCC AATAAGCCTT CTGTCGCCGT CAGAGTGCTG 780
 229 S W G Y V P C G T P N K P S V A V R V L 248
 781 TCTTATGTGA AGTGGATCGA GGACACCATA GCGGAGAACT CCTGAACGCC CAGCCCTGTC 840
 249 S Y V K W I E D T I A E N S * 262
 841 CCCTACCCCC AGTAAATCA AATGTGCATC C 871

Figure 25A

1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

 61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

 121 GTGCTGCCGA CATTTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTG 180
 39 V L P T F I I S I C F F G L L G N L F V 58

 181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

 241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

 301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAATGG GGTCATCAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

 361 GCCAATTTGT TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

 421 CTGGTGACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTCACCTGC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

 481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCTGTCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

 541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I L L L P H E A W 198

 601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

 661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

 721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

 781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

 841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

[illegible]

1081 CC 1082

1081 CC 1082

Figure 26A

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1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1      M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTCAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACT CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GACAGGCCCC GGTACCTGTC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 26B

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901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

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Figure 27A

1 CTGTGCATGG CATCATCCTG GCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
 1 M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
 19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTG 180
 39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
 59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGGCAGA GAATATCTGG 300
 79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTAAG 360
 99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTTGT TCATCAGCAT CTTCCTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
 119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGACCT CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
 139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
 159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCTGTC TCCTCCCCCA TGAGGCCTGG 600
 179 Q A V P D L N I T A C I V L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
 199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
 219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
 239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
 259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
 279 Q A V R G C F W E D F I D L G L Q L A N 298

Figure 27B

901 TTCTTTGCCT TCACTAACAG CTCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

1081 CC 1082

Figure 28A

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1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1      M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGTC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCACTAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCTTGGTG GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCAAC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGCATCCTGC TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R K E V S R T 238

721 AGAGTGGGGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R V R G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGAATTTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCTT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 28B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

1081 CC 1082

Figure 29A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC 60
1 M F S P W K I S M F L S V C E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTCCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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Figure 29B

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901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGTGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
381 H K L Q D W A G S R Q * 391

1201 AATTGTGTAT AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCAATTTTGG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAATCAC AACAGCATT CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCCTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACCT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACCTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

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Figure 29C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTG CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
2281 CCACCTTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTCTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCAC CACCAGCCGG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CTTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

Figure 29D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAA CAGGTGAAAG AAGAAGTAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAACTGTGC CACACATGGT GAATGAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACAC GGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAA AAA 3733

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3721
3733

Figure 30A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTC GTGAGGACTC CGTGCCCACC 60
1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCCT GAGTGTCATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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Figure 30B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GACGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

 1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTGTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCAGGAA TGCCAAGGAG 1260

 1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

 1321 TCCTGCCCTG CCCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

 1381 GCCAAGGACT CCAAATCAC AACAGCATT CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

 1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

 1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

 1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

 1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATTA ATAAAGGTTA AGCCCTGAGG 1680

 1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

 1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

 1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

 1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCTG ACGAGACGGT 1920

 1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

 1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 30C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTÀ CGCAGACGTA ACTGGGATAT GTTACTATA ÀGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATT TGGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTC AATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

Figure 30D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTAG TATTAGTATT 3360
3361 AGAATGAAGT CAAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAA AAA 3733

Figure 31A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGACTC CGTGCCCACC 60
1 M F S P W K I S M F L S V R E D S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTT GAGTGTCATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

```

Figure 31B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTG CCAGGGAGTG TGCCAGAAAG AGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K E G C R S E P 360

1081 ATTCAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTG AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCAATTTTGG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CCAAAATCAC AACAGCATTA CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAACT TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 31C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTÀ CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTÀ GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAAGCGT GAAAAAAAAG 3240

Figure 31D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

3241
3301
3361
3421
3481
3541
3601
3661
3721
3733

Figure 32A

1 CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAAATCTCATGAGGAGGTTTTAGTCTA 60
 61 GGGAAAGTCATTTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG 120
 1 M S S S S W 6
 121 GCTCCTTCTCAGCCTTGTTGCTGTAAGTCTGCTCAGTCCACCATTGAGGAACAGGCCAA 180
 7 L L L S L V A V T A A Q S T I E E Q A K 26
 181 GACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC 240
 27 T F L D K F N H E A E D L F Y Q S S L A 46
 241 TTCTTGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG 300
 47 S W N Y N T N I T E E N V Q N M N N A G 66
 301 GGACAAATGGTCTGCCTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA 360
 67 D K W S A F L K E Q S T L A Q M Y P L Q 86
 361 AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC 420
 87 E I Q N L T V K L Q L Q A L Q Q N G S S 106
 421 AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT 480
 107 V L S E D K S K R L N T I L N T M S T I 126
 481 CTACAGTACTGGAAAAGTTTGTAAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC 540
 127 Y S T G K V C N P D N P Q E C L L L E P 146
 541 AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA 600
 147 G L N E I M A N S L D Y N E R L W A W E 166
 601 AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT 660
 167 S W R S E V G K Q L R P L Y E E Y V V L 186
 661 GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA 720
 187 K N E M A R A N H Y E D Y G D Y W R G D 206
 721 CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGGCCAGTTGATTGAAGATGT 780
 207 Y E V N G V D G Y D Y S R G Q L I E D V 226
 781 GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC 840
 227 E H T F E E I K P L Y E H L H A Y V R A 246
 841 AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATTT 900
 247 K L M N A Y P S Y I S P I G C L P A H L 266

Figure 32B

901	GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCTTTGG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAAATTCATGCTAACGGACCCAGGAAATGTTTCAGAAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTTCATTCGATATTACACAAGGACCCCTTACCAATTCCAGTTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

Figure 32C

1741	CTCTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTGGAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAACAAAGAATTCTTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTTGAGATAAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAAATGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAATAATCCAGGATTCCAAACACTGATGATGTTTCAGACCTCCTTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTTTCTCTTGAGGTGATTTTGTGTATGTAAATGTTAATTTTCATGG	2580
2581	TATAGAAAATATAAGATGATAAAGATATCATTAATGTCAAAACTATGACTCTGTTCAGA	2640

Figure 32D

2641 AAAAAAATTGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC 2700
2701 AGTATTTATTTCTGTCTCTGGATTTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT 2760
2761 TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAAT 2820
2821 GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTG 2880
2881 GATCTTGTATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAAGTGGTGTAGC 2940
2941 TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTTCATTTAATCCATTGTCAAGGATGA 3000
3001 CATGCTTTCTTCACAGTAACTCAGTTCAAGTACTATGGTGATTTGCCTACAGTGATGTTT 3060
3061 GGAATCGATCATGCTTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG 3120
3121 GTAGAGGACATTGCTTTTTCTACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA 3180
3181 AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAACTCATTTCTAC 3240
3241 TGTCTCTAACTGTGGAGTGAATGGAAATTCCTCAACTGTATGTTTACCCTCTGAAGTGGGT 3300
3301 ACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGTTTGAGCAGTGCTGAGCACAAAG 3360
3361 CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAAA 3405

Figure 33A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTTCATTTTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 33B

841 CCTAACCAAGGCAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
281 P N Q G K M R E I E E V L T P E M L M R 300

901 TGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCAAG 960
301 W N N L L R K R N F Y K K L E L H L P K 320

961 TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT 1020
321 F S I S G S Y V L D Q I L P R L G F T D 340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC 1080
341 L F S K W A D L S G I T K Q Q K L E A S 360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCAGGCTGCAGCAGCC 1140
361 K S F H K A T L D V D E A G T E A A A A 380

1141 ACCACGTTTCGCGATCAAATTCCTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC 1200
381 T T F A I K F F S A Q T N R H I L R F N 400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG 1260
401 R P F L V V I F S T S T Q S V L F L G K 420

1261 GTCGTCGACCCACGAAACCATAG 1284
421 V V D P T K P * 428

Figure 34A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCACTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTTCATTTTCCTCAAGGACCACTCCCAAAGACTTTTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 34B

841 CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
281 P N Q G K M R E I E E V L T P E M L M R 300

901 TGGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCAAG 960
301 W N N L L R K R N F Y K K L E L H L P K 320

961 TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT 1020
321 F S I S G S Y V L D Q I L P R L G F T D 340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC 1080
341 L F S K W A D L S G I T K Q Q K L E A S 360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC 1140
361 K S F H K A T L D V D E A G T E A A A A 380

1141 ACCACGTTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC 1200
381 T T F A I K F F S A Q T N R H I L R F N 400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG 1260
401 R P F L V V I F S T S T Q S V L F L G K 420

1261 GTCGTCGACCCACGAAACCATAG 1284
421 V V D P T K P * 428

Figure 35A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTCAGCGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 35B

841 CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
281 P N Q G K M R E I E E V L T P E M L M R 300

901 TGGAACAACCTTGTTCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG 960
301 W N N L L R K R N F Y K K L E L H L P K 320

961 TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT 1020
321 F S I S G S Y V L D Q I L P R L G F T D 340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACCTGGAGGCATCC 1080
341 L F S K W A D L S G I T K Q Q K L E A S 360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCAGGCTGCAGCAGCC 1140
361 K S F H K A T L D V D E A G T E A A A A 380

1141 ACCACGTTTCGCGATCAAATCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC 1200
381 T T F A I K F F S A Q T N R H I L R F N 400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG 1260
401 R P F L V V I F S T S T Q S V L F L G K 420

1261 GTCGTCGACCCACGAAACCATAG 1284
421 V V D P T K P * 428

Figure 36A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCCTACGCCATGCTTTCCCTGGGGGCGCTCACACAGCCGAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTTCAGNGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTTCATTTCTCAAGGACCACTCCCAAAGACTTNTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 36B

841 CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
281 P N Q G K M R E I E E V L T P E M L M R 300

901 TGGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG 960
301 W N N L L R K R N F Y K K L E L H L P K 320

961 TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT 1020
321 F S I S G S Y V L D Q I L P R L G F T D 340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACCTGGAGGCATCC 1080
341 L F S K W A D L S G I T K Q Q K L E A S 360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC 1140
361 K S F H K A T L D V D E A G T E A A A A 380

1141 ACCACGTTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC 1200
381 T T F A I K F F S A Q T N R H I L R F N 400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG 1260
401 R P F L V V I F S T S T Q S V L F L G K 420

1261 GTCGTCGACCCACGAAACCATAG 1284
421 V V D P T K P * 428

Figure 37A

1	CGCCCAACCCAAGTTCAAAGGCTGATAAGAGAGAAAAATCTCATGAGGAGGTTTTAGTCTA	60
61	GGGAAAGTCATTTCAGTGGATGTGATCTTGGCTCACAGGGGACGATGTCAAGCTCTTCCTG	120
1	M S S S S W	6
121	GCTCCTTCTCAGCCTTGTTGCTGTAAGTCTGCTCAGTCCACCATTGAGGAACAGGCCAA	180
7	L L L S L V A V T A A Q S T I E E Q A K	26
181	GACATTTTTGGACAAGTTTAACCACGAAGCCGAAGACCTGTTCTATCAAAGTTCACTTGC	240
27	T F L D K F N H E A E D L F Y Q S S L A	46
241	TTCTTGGAATTATAACACCAATATTACTGAAGAGAATGTCCAAAACATGAATAATGCTGG	300
47	S W N Y N T N I T E E N V Q N M N N A G	66
301	GGACAAATGGTCTGCCTTTTTTAAAGGAACAGTCCACACTTGCCCAAATGTATCCACTACA	360
67	D K W S A F L K E Q S T L A Q M Y P L Q	86
361	AGAAATTCAGAATCTCACAGTCAAGCTTCAGCTGCAGGCTCTTCAGCAAAATGGGTCTTC	420
87	E I Q N L T V K L Q L Q A L Q Q N G S S	106
421	AGTGCTCTCAGAAGACAAGAGCAAACGGTTGAACACAATTCTAAATACAATGAGCACCAT	480
107	V L S E D K S K R L N T I L N T M S T I	126
481	CTACAGTACTGGAAAAGTTTGTAACCCAGATAATCCACAAGAATGCTTATTACTTGAACC	540
127	Y S T G K V C N P D N P Q E C L L L E P	146
541	AGGTTTGAATGAAATAATGGCAAACAGTTTAGACTACAATGAGAGGCTCTGGGCTTGGGA	600
147	G L N E I M A N S L D Y N E R L W A W E	166
601	AAGCTGGAGATCTGAGGTCGGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGTCTT	660
167	S W R S E V G K Q L R P L Y E E Y V V L	186
661	GAAAAATGAGATGGCAAGAGCAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGA	720
187	K N E M A R A N H Y E D Y G D Y W R G D	206
721	CTATGAAGTAAATGGGGTAGATGGCTATGACTACAGCCGCGCCAGTTGATTGAAGATGT	780
207	Y E V N G V D G Y D Y S R G Q L I E D V	226
781	GGAACATACCTTTGAAGAGATTAAACCATTATATGAACATCTTCATGCCTATGTGAGGGC	840
227	E H T F E E I K P L Y E H L H A Y V R A	246
841	AAAGTTGATGAATGCCTATCCTTCCTATATCAGTCCAATTGGATGCCTCCCTGCTCATT	900
247	K L M N A Y P S Y I S P I G C L P A H L	266

Figure 37B

901	GCTTGGTGATATGTGGGGTAGATTTTGGACAAATCTGTACTCTTTGACAGTTCCTTTGG	960
267	L G D M W G R F W T N L Y S L T V P F G	286
961	ACAGAAACCAACATAGATGTTACTGATGCAATGGTGGACCAGGCCTGGGATGCACAGAG	1020
287	Q K P N I D V T D A M V D Q A W D A Q R	306
1021	AATATTCAAGGAGGCCGAGAAGTTCTTTGTATCTGTTGGTCTTCCTAATATGACTCAAGG	1080
307	I F K E A E K F F V S V G L P N M T Q G	326
1081	ATTCTGGGAAAATTCCATGCTAACGGACCCAGGAAATGTTTCAGAAAGCAGTCTGCCATCC	1140
327	F W E N S M L T D P G N V Q K A V C H P	346
1141	CACAGCTTGGGACCTGGGGAAGGGCGACTTCAGGATCCTTATGTGCACAAAGGTGACAAT	1200
347	T A W D L G K G D F R I L M C T K V T M	366
1201	GGACGACTTCCTGACAGCTCATCATGAGATGGGGCATATCCAGTATGATATGGCATATGC	1260
367	D D F L T A H H E M G H I Q Y D M A Y A	386
1261	TGCACAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCCATGAAGCTGTTGGGGA	1320
387	A Q P F L L R N G A N E G F H E A V G E	406
1321	AATCATGTCACTTTCTGCAGCCACACCTAAGCATTTAAAATCCATTGGTCTTCTGTCACC	1380
407	I M S L S A A T P K H L K S I G L L S P	426
1381	CGATTTTCAAGAAGACAATGAAACAGAAATAAACTTCCTGCTCAAACAAGCACTCACGAT	1440
427	D F Q E D N E T E I N F L L K Q A L T I	446
1441	TGTTGGGACTCTGCCATTTACTTACATGTTAGAGAAGTGGAGGTGGATGGTCTTTAAAGG	1500
447	V G T L P F T Y M L E K W R W M V F K G	466
1501	GGAAATTCCCAAAGACCAGTGGATGAAAAAGTGGTGGGAGATGAAGCGAGATAGTTGG	1560
467	E I P K D Q W M K K W W E M K R E I V G	486
1561	GGTGGTGGAAACCTGTGCCCCATGATGAAACATACTGTGACCCCGCATCTCTGTTCCATGT	1620
487	V V E P V P H D E T Y C D P A S L F H V	506
1621	TTCTAATGATTACTCATTCATTCGATATTACACAAGGACCCTTTACCAATTCCAGTTTCA	1680
507	S N D Y S F I R Y Y T R T L Y Q F Q F Q	526
1681	AGAAGCACTTTGTCAAGCAGCTAAACATGAAGGCCCTCTGCACAAATGTGACATCTCAAA	1740
527	E A L C Q A A K H E G P L H K C D I S N	546

Figure 37C

1741	CTCTACAGAAGCTGGACAGAACTGTTCAATATGCTGAGGCTTGGAAAATCAGAACCCCTG	1800
547	S T E A G Q K L F N M L R L G K S E P W	566
1801	GACCCTAGCATTTGAAAAATGTTGTAGGAGCAAAGAACATGAATGTAAGGCCACTGCTCAA	1860
567	T L A L E N V V G A K N M N V R P L L N	586
1861	CTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAGAAACAAGAATTCTTTTGTGGGATG	1920
587	Y F E P L F T W L K D Q N K N S F V G W	606
1921	GAGTACCGACTGGAGTCCATATGCAGACCAAAGCATCAAAGTGAGGATAAGCCTAAAATC	1980
607	S T D W S P Y A D Q S I K V R I S L K S	626
1981	AGCTCTTGGAGATAAAGCATATGAATGGAACGACAATGAAATGTACCTGTTCCGATCATC	2040
627	A L G D K A Y E W N D N E M Y L F R S S	646
2041	TGTTGCATATGCTATGAGGCAGTACTTTTTAAAAGTAAAAAATCAGATGATTCTTTTGG	2100
647	V A Y A M R Q Y F L K V K N Q M I L F G	666
2101	GGAGGAGGATGTGCGAGTGGCTAATTTGAAACCAAGAATCTCCTTTAATTTCTTTGTCAC	2160
667	E E D V R V A N L K P R I S F N F F V T	686
2161	TGCACCTAAAAACGTGTCTGATATCATTCCTAGAACTGAAGTTGAAAAGGCCATCAGGAT	2220
687	A P K N V S D I I P R T E V E K A I R M	706
2221	GTCCCGGAGCCGTATCAATGATGCTTTCCGTCTGAATGACAACAGCCTAGAGTTTCTGGG	2280
707	S R S R I N D A F R L N D N S L E F L G	726
2281	GATACAGCCAACACTTGGACCTCCTAACCAGCCCCCTGTTTCCATATGGCTGATTGTTTT	2340
727	I Q P T L G P P N Q P P V S I W L I V F	746
2341	TGGAGTTGTGATGGGAGTGATAGTGGTTGGCATTGTCATCCTGATCTTCACTGGGATCAG	2400
747	G V V M G V I V V G I V I L I F T G I R	766
2401	AGATCGGAAGAAGAAAAATAAAGCAAGAAGTGGAGAAAATCCTTATGCCTCCATCGATAT	2460
767	D R K K K N K A R S G E N P Y A S I D I	786
2461	TAGCAAAGGAGAAAAATAATCCAGGATTCCAAAACACTGATGATGTTTCAGACCTCCTTTTA	2520
787	S K G E N N P G F Q N T D D V Q T S F *	806
2521	GAAAAATCTATGTTTTTCCTCTTGAGGTGATTTTGTGTATGTAAATGTTAATTCATGG	2580
2581	TATAGAAAATATAAGATGATAAAGATATCATTAATGTCAAAACTATGACTCTGTTCAGA	2640

Figure 37D

2641 AAAAAAATGTCCAAAGACAACATGGCCAAGGAGAGAGCATCTTCATTGACATTGCTTTC 2700
2701 AGTATTTATTTCTGTCTCTGGATTTGACTTCTGTTCTGTTTCTTAATAAGGATTTTGTAT 2760
2761 TAGAGTATATTAGGGAAAGTGTGTATTTGGTCTCACAGGCTGTTTCAGGGATAATCTAAAT 2820
2821 GTAAATGTCTGTTGAATTTCTGAAGTTGAAAACAAGGATATATCATTGGAGCAAGTGTG 2880
2881 GATCTTGATATGGAATATGGATGGATCACTTGTAAGGACAGTGCCTGGGAACGGTGTAGC 2940
2941 TGCAAGGATTGAGAATGGCATGCATTAGCTCACTTTCATTTAATCCATTGTCAAGGATGA 3000
3001 CATGCTTCTTTCACAGTAACTCAGTTCAAGTACTATGGTGATTGCTTACAGTGATGTTT 3060
3061 GGAATCGATCATGCTTCTTCAAGGTGACAGGTCTAAAGAGAGAAGAATCCAGGGAACAG 3120
3121 GTAGAGGACATTGCTTTTTTCACTTCCAAGGTGCTTGATCAACATCTCCCTGACAACACAA 3180
3181 AACTAGAGCCAGGGGCCTCCGTGAACTCCCAGAGCATGCCTGATAGAACTCATTCTTCTAC 3240
3241 TGTCTCTAACTGTGGAGTGAATGGAAATTCCAAGTGTATGTTTACCCTCTGAAGTGGGT 3300
3301 ACCCAGTCTCTTAAATCTTTTGTATTTGCTCACAGTGTTTGAGCAGTGCTGAGCACAAAG 3360
3361 CAGACACTCAATAAATGCTAGATTTACACACTCAAAAAAAAAAAAA 3405

Figure 38A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTN GTGAGGNCTC CGTGCCCAAC 60
1 M F S P W K I S M F L S V X E X S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTCC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTTCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTCA CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCTT GAGTGTATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTCATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

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Figure 38B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GANGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

 961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

 1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG NGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K X G C R S E P 360

 1081 ATTACAGATGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

 1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

 1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCAGGAA TGCCAAGGAG 1260

 1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAAACACC GGAGACTAAT 1320

 1321 TCCTGCCCTG CCAATTTTG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

 1381 GCCAAGGACT CCAAAATCAC AACAGCATT CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

 1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

 1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAAC TATAGCTCCA GGAGAACTGC 1560

 1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTTCTTTAA 1620

 1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCATTA ATAAAGGTTA AGCCCTGAGG 1680

 1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

 1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

 1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

 1861 AAGACTCAAG TGGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCG ACGAGACGGT 1920

 1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

 1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 38C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
 2101 GTACATGTGA GGCATCATTA CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
 2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
 2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
 2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
 2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
 2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGGAGAGT GCAGGCCTGC 2460
 2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
 2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
 2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
 2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
 2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
 2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
 2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
 2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
 2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
 3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
 3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
 3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
 3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

Figure 38D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TTCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAAA CAGGTGAAAG AAGAAGTAAA AACCATTAG TATTAGTATT 3360
3361 AGAATGAAGT CAACTGTGC CACACATGGT GAATGAAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGTA AACAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAAA AAA 3733

E0053 NP

D0053 NP

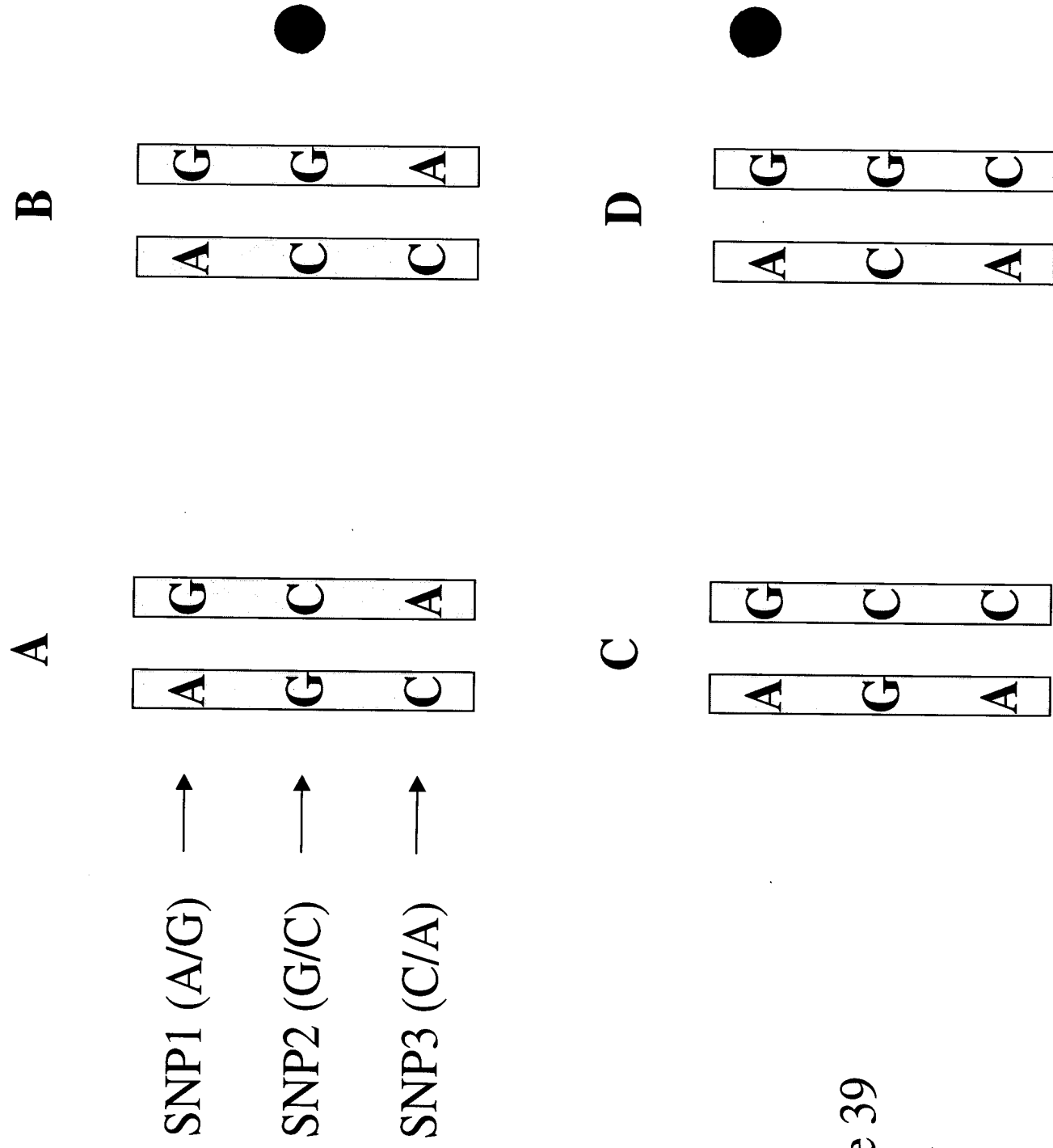


Figure 39

D0053 NP

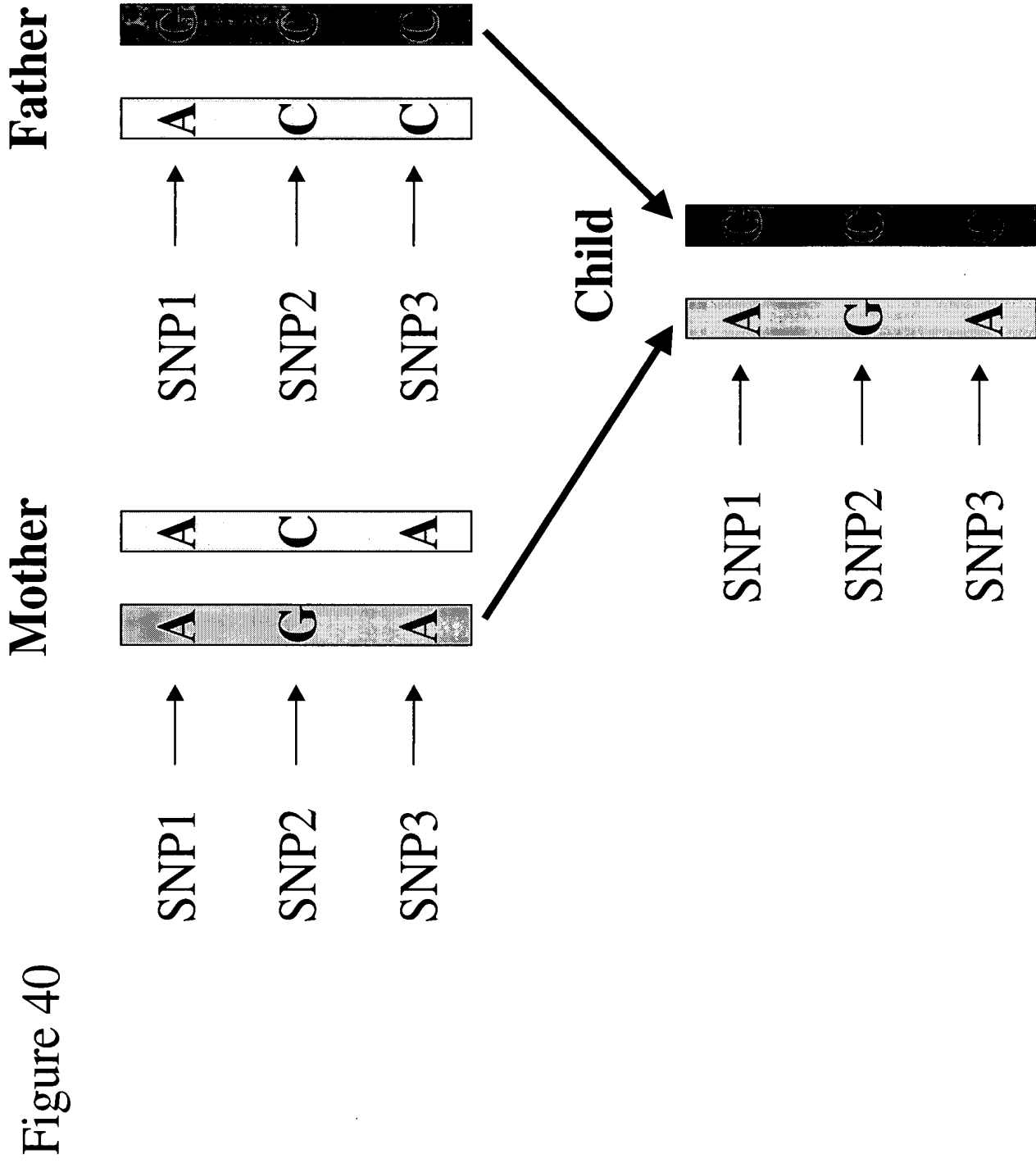


Figure 41A

1 CACCCTATCC TACTACTACTA GGAAGTTGCA CAGTCCGCCT CGGGCAGCCC AAAGTCCTCT 60
 61 TCCCCACCCT GGCTCCCAAA ACCCTCCAAA ACAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCCACCCTC TGTCTGCTCG AGCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGCTC CTCCATCCAC 240
 241 CCAGCGCCGG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCA CCCCCCTTAC CTTCCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCGTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAAGTGA GTGGTGAATA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC TGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGCTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTTGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 41B

961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
 233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCTTACA CGCTGCTCAC AGACTCTTCT 1080
 253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAAGTCC 1140
 273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCTG TGACAGCATC 1200
 293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
 313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
 333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
 353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
 373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCTCTC 1500
 393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
 413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
 433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCCTCT 1680
 453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
 473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
 493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
 513 D A G L N Y G H G T G H G I G N F L C V 532

Figure 41C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCCGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGA CATGGAACCC ATGATTCCTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

Figure 41D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTTGGAG AACAAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTCTTTGG ATGCCCTTTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTCCTCCA TTTTACAGAC AGGAAAAGTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTC CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

Figure 42A

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1 CTGTGCATGG CATCATCCTG GCCCCCTCTA GAGCTCCAAT CCTCCAACCA GAGCCAGCTC 60
1      M A S S W P P L E L Q S S N Q S Q L 18

61 TTCCCTCAA ATGCTACGGC CTGTGACAAT GCTCCAGAAG CCTGGGACCT GCTGCACAGA 120
19 F P Q N A T A C D N A P E A W D L L H R 38

121 GTGCTGCCGA CATTATCAT CTCCATCTGT TTCTTCGGCC TCCTAGGGAA CCTTTTGTGC 180
39 V L P T F I I S I C F F G L L G N L F V 58

181 CTGTTGGTCT TCCTCCTGCC CCGGCGGCAA CTGAACGTGG CAGAAATCTA CCTGGCCAAC 240
59 L L V F L L P R R Q L N V A E I Y L A N 78

241 CTGGCAGCCT CTGATCTGGT GTTTGTCTTG GGCTTGCCCT TCTGGGCAGA GAATATCTGG 300
79 L A A S D L V F V L G L P F W A E N I W 98

301 AACCAGTTTA ACTGGCCTTT CGGAGCCCTC CTCTGCCGTG TCATCAACGG GGTCAACAAG 360
99 N Q F N W P F G A L L C R V I N G V I K 118

361 GCCAATTGTG TCATCAGCAT CTTCTCTGGT GTGGCCATCA GCCAGGACCG CTACCGCGTG 420
119 A N L F I S I F L V V A I S Q D R Y R V 138

421 CTGGTGCACC CTATGGCCAG CGGAAGGCAG CAGCGGCGGA GGCAGGCCCG GGTACCTGTC 480
139 L V H P M A S G R Q Q R R R Q A R V T C 158

481 GTGCTCATCT GGGTTGTGGG GGGCCTCTTG AGCATCCCCA CATTCCTGCT GCGATCCATC 540
159 V L I W V V G G L L S I P T F L L R S I 178

541 CAAGCCGTCC CAGATCTGAA CATCACCGCC TGATCCTGCT TCCTCCCCCA TGAGGCCTGG 600
179 Q A V P D L N I T A C I L L L P H E A W 198

601 CACTTTGCAA GGATTGTGGA GTTAAATATT CTGGGTTTCC TCCTACCACT GGCTGCGATC 660
199 H F A R I V E L N I L G F L L P L A A I 218

661 GTCTTCTTCA ACTACCACAT CCTGGCCTCC CTGCGAACGC GGGAGGAGGT CAGCAGGACA 720
219 V F F N Y H I L A S L R T R E E V S R T 238

721 AGAGTGCAGG GGCCGAAGGA TAGCAAGACC ACAGCGCTGA TCCTCACGCT CGTGGTTGCC 780
239 R V Q G P K D S K T T A L I L T L V V A 258

781 TTCCTGGTCT GCTGGGCCCC TTACCACTTC TTTGCCTTCC TGGAATTCTT ATTCCAGGTG 840
259 F L V C W A P Y H F F A F L E F L F Q V 278

841 CAAGCAGTCC GAGGCTGCCT TTGGGAGGAC TTCATTGACC TGGGCCTGCA ATTGGCCAAC 900
279 Q A V R G C F W E D F I D L G L Q L A N 298

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Figure 42B

901 TTCTTTGCCT TCACTAACAG CTCCCTGAAT CCAGTAATTT ATGTCTTTGT GGGCCGGCTC 960
299 F F A F T N S S L N P V I Y V F V G R L 318

961 TTCAGGACCA AGGTCTGGGA ACTTTATAAA CAATGCACCC CTAAAAGTCT TGCTCCAATA 1020
319 F R T K V W E L Y K Q C T P K S L A P I 338

1021 TCTTCATCCC ATAGGAAAGA AATCTTCCAA CTTTCTGGC GGAATTAAAA CAGCATTGAA 1080
339 S S S H R K E I F Q L F W R N * 353

1081 CC 1082

1081 CC 1082

Figure 43A

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1 ATGTTCTCTC CCTGGAAGAT ATCAATGTTT CTGTCTGTTT GTGAGGCCTC CGTGCCCAACC 60
1 M F S P W K I S M F L S V R E A S V P T 20

61 ACGGCCTCTT TCAGCGCCGA CATGCTCAAT GTCACCTTGC AAGGGCCAC TCTTAACGGG 120
21 T A S F S A D M L N V T L Q G P T L N G 40

121 ACCTTTGCC AGAGCAAATG CCCCCAAGTG GAGTGGCTGG GCTGGCTCAA CACCATCCAG 180
41 T F A Q S K C P Q V E W L G W L N T I Q 60

181 CCCCCCTTC TCTGGGTGCT GTTCGTGCTG GCCACCCTAG AGAACATCTT TGTCTCAGC 240
61 P P F L W V L F V L A T L E N I F V L S 80

241 GTCTTCTGCC TGCACAAGAG CAGCTGCACG GTGGCAGAGA TCTACCTGGG GAACCTGGCC 300
81 V F C L H K S S C T V A E I Y L G N L A 100

301 GCAGCAGACC TGATCCTGGC CTGCGGGCTG CCCTTCTGGG CCATCACCAT CTCCAACAAC 360
101 A A D L I L A C G L P F W A I T I S N N 120

361 TTCGACTGGC TCTTTGGGGA GACGCTCTGC CGCGTGGTGA ATGCCATTAT CTCCATGAAC 420
121 F D W L F G E T L C R V V N A I I S M N 140

421 CTGTACAGCA GCATCTGTTT CCTGATGCTG GTGAGCATCG ACCGCTACCT GGCCCTGGTG 480
141 L Y S S I C F L M L V S I D R Y L A L V 160

481 AAAACCATGT CCATGGGCCG GATGCGCGGC GTGCGCTGGG CCAAGCTCTA CAGCTTGGTG 540
161 K T M S M G R M R G V R W A K L Y S L V 180

541 ATCTGGGGGT GTACGCTGCT CCTGAGCTCA CCCATGCTGG TGTCCGGAC CATGAAGGAG 600
181 I W G C T L L L S S P M L V F R T M K E 200

601 TACAGCGATG AGGGCCACAA CGTCACCGCT TGTGTCATCA GCTACCCATC CCTCATCTGG 660
201 Y S D E G H N V T A C V I S Y P S L I W 220

661 GAAGTGTTC CCAACATGCT CCTGAATGTC GTGGGCTTCC TGCTGCCCT GAGTGTATC 720
221 E V F T N M L L N V V G F L L P L S V I 240

721 ACCTTCTGCA CGATGCAGAT CATGCAGGTG CTGCGGAACA ACGAGATGCA GAAGTTCAAG 780
241 T F C T M Q I M Q V L R N N E M Q K F K 260

781 GAGATCCAGA CGAGAGGAG GGCCACGGTG CTAGTCCTGG TTGTGCTGCT GCTATTATC 840
261 E I Q T E R R A T V L V L V V L L L F I 280

841 ATCTGCTGGC TGCCCTTCCA GATCAGCACC TTCCTGGATA CGCTGCATCG CCTCGGCATC 900
281 I C W L P F Q I S T F L D T L H R L G I 300

```

Figure 43B

901 CTCTCCAGCT GCCAGGACGA GCGCATCATC GATGTAATCA CACAGATCGC CTCCTTCATG 960
 301 L S S C Q D E R I I D V I T Q I A S F M 320

961 GCCTACAGCA ACAGCTGCCT CAACCCACTG GTGTACGTGA TCGTGGGCAA GCGCTTCCGA 1020
 321 A Y S N S C L N P L V Y V I V G K R F R 340

1021 AAGAAGTCTT GGGAGGTGTA CCAGGGAGTG TGCCAGAAAG GGGGCTGCAG GTCAGAACCC 1080
 341 K K S W E V Y Q G V C Q K G G C R S E P 360

1081 ATTCAAGTGG AGAACTCCAT GGGCACACTG CGGACCTCCA TCTCCGTGGA ACGCCAGATT 1140
 361 I Q M E N S M G T L R T S I S V E R Q I 380

1141 CACAACTGC AGGACTGGGC AGGGAGCAGA CAGTGAGCAA ACGCCAGCAG GGCTGCTGTG 1200
 381 H K L Q D W A G S R Q * 391

1201 AATTTGTGTA AGGATTGAGG GACAGTTGCT TTTCAGCATG GGCCAGGAA TGCCAAGGAG 1260

1261 ACATCTATGC ACGACCTTGG GAAATGAGTT GATGTCTCCG GTAAACACC GGAGACTAAT 1320

1321 TCCTGCCCTG CCAATTTTGG CAGGGAGCAT GGCTGTGAGG ATGGGGTGAA CTCACGCACA 1380

1381 GCCAAGGACT CAAAATCAC AACAGCATT CTGTTCTTAT TTGCTGCCAC ACCTGAGCCA 1440

1441 GCCTGCTCCT TCCCAGGAGT GGAGGAGGCC TGGGGGGAGG GAGAGGAGTG ACTGAGCTTC 1500

1501 CCTCCCGTGT GTTCTCCGTC CCTGCCCCAG CAAGACAAC TAGATCTCCA GGAGAACTGC 1560

1561 CATCCAGCTT TGGTGCAATG GCTGAGTGCA CAAGTGAGTT GTTGCCCTGG GTTCTTTTAA 1620

1621 TCTATTCAGC TAGAACTTTG AAGGACAATT TCTTGCAATTA ATAAAGGTTA AGCCCTGAGG 1680

1681 GGTCCCTGAT AACAACTGG AGACCAGGAT TTTATGGCTC CCCTCACTGA TGGACAAGGA 1740

1741 GGTCTGTGCC AAAGAAGAAT CCAATAAGCA CATATTGAGC ACTTGCTGTA TATGCAGTAT 1800

1801 TGAGCACTGT AGGCAAGACC CAAGAAAGAG AAGGAGCCAT CTCCATCTTG AAGGAACTCA 1860

1861 AAGACTCAAG TGGAACGAC TGGGCACTGC CACCACCAGA AAGCTGTTCTG ACGAGACGGT 1920

1921 CGAGCAGGGT GCTGTGGGTG ATATGGACAG CAGAAGGGGG AGACCAAGGT TCCAGCTCAA 1980

1981 CCAATAACTA TTGCACAACC ACCTGTCCCT GCCTCAGTTC CCTTTTATGT AACATGAAGT 2040

Figure 43C

2041 CGTTGTGAGG GTTAAAGGCA GTAACAGGTA TAAAGTACTT AGAAAAGCAA AGGGTGCTAC 2100
2101 GTACATGTGA GGCATCATTG CGCAGACGTA ACTGGGATAT GTTTACTATA AGGAAAAGAC 2160
2161 ACTGAGGTCT AGAAATAGCT CCGTGGAGCA GAATCAGTAT TGGGAGCCGG TGGCGGTGTG 2220
2221 AAGCACCAGT GTCTGGCACA CAGTAGGTGC TCATTGGCTC CCTTCCACCT GTCATTCCCA 2280
2281 CCACCCTGAG GCCCCAACCG CCACACACAC AGGAGCATTT GGAGAGAAGG CCATGTCTTC 2340
2341 AAAGTCTGAT TTGTGATGAG GCAGAGGAAG ATATTTCTAA TCGGTCTTGC CCAGAGGATC 2400
2401 ACAGTGCTGA GACCCCCCAC CACCAGCCGG TACCTGGGAA GGGGAGAGT GCAGGCCTGC 2460
2461 TCAGGGACTG TTCCTGTCTC AGCAACCAAG GGATTGTTCC TGTCAATCAA TGGTTTATTG 2520
2521 GAAGGTGGCC CAGTATGAGC CCTAGAAGAG TGTGAAAAGG AATGGCAATG GTGTTCACCA 2580
2581 TCGGCAGTGC CAGGGCAGCA CTCATTCACT TGATAAATGA ATATTTATTA GCTGGTTGGA 2640
2641 GAGCTAGAAC CTGGAGAGCT AGAACCTGGA GAACTAGAAC CTGGAGGGCT AGAACCTGGA 2700
2701 GAGGCTAGAA CCAAGAAGGG CTAGAACCTG GAGGGGCTAG AACCTAGAGA AGCTAAAACC 2760
2761 TGAGCTAGAA GCTGGAGGAC TAGAACCTGG AGGGCTGGAA TCTGAAGGGC TAGAACCTGG 2820
2821 AGGGCTGGAA TCTGGAGAGC TAGAACCTGG AGGGCTAGAA CCTGGAGGGC TAGAACCTAG 2880
2881 AAGGGCTAGA ACCTGGAGGG CTGGAATCTG GAGAGCTAGA ACCTGGAGGG CTAGAACCTG 2940
2941 GAGGGCTAGA ACCTAGAAGG GCTAGAACCT GGAGGGCTAG AACCTGGCAG GTTAGAACCT 3000
3001 AGAAGGGCTA GAACCTGGAG AGCCAGAACC TGGAGGGCTA GAACCTGGAA GGGCTAGAAC 3060
3061 CTGTAGAGCT AGAACATGGA GAGCTAGAAC CCGCAGGCT AGAACCTGGC AAGCTAGAAC 3120
3121 CTGGAGGGAA TGAACCTGGA GGGCTAGAAC CTGGAGAATG AGAAAAATTT ACATGGCAAA 3180
3181 GAGCCCATAA ATCCTGACCA ATCCAACCTCT GAATTTTAAA GCAAAAGCGT GAAAAAAAAG 3240

Figure 43D

3241 ATTCCCTCCT TACCCCAAC CCACTCTTTT TCCCACCAC CCACTCTCCT CTGCCTCAGT 3300
3301 AAGTATCTGG AGGAAGAAA CAGGTGAAAG AAGAAGTAAA AACCATTTAG TATTAGTATT 3360
3361 AGAATGAAGT CAACTGTGC CACACATGGT GAATGAAAA AAAAAAAG AGGCTGTGTT 3420
3421 TTGTCACACA GGCAGTCAT TCAGCACCAG AGCACGTGAT GGTCTGAGAC TCTCTTAGGA 3480
3481 GCAGAGCTCT GCCGCAATGG CCATGTGGGG ATCCACACCT GGTCTGAGGG GCAACTGAGT 3540
3541 CTGCGGGAGA AGAGCGGCC TATGCATGGT GTAGATGCCC TGATAAAGAA CATCTGTCCT 3600
3601 GTGAAAGACT CAATGAGCTG TTATGTTGT AAGAGGAAGC ATTTACATC CAAACGAGAA 3660
3661 AATCATGTAA ACATGTGTCT TTTCTGTAGA GCATAATAAA TGGATGAGGT TTTTGCAAAA 3720
3721 AAAAAAAAA AAA 3733

Figure 44A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACACGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T R V G	140
421	AGTGCTCTGTTCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTTGGTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 44B

841 CCTAACCAAGGCAAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
281 P N Q G K M R E I E E V L T P E M L M R 300

901 TGGAACAACCTTGTTGCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCCAAG 960
301 W N N L L R K R N F Y K K L E L H L P K 320

961 TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT 1020
321 F S I S G S Y V L D Q I L P R L G F T D 340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACCTGGAGGCATCC 1080
341 L F S K W A D L S G I T K Q Q K L E A S 360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCAGGCTGCAGCAGCC 1140
361 K S F H K A T L D V D E A G T E A A A A 380

1141 ACGACGTTTCGCGATCAAATTTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC 1200
381 T T F A I K F F S A Q T N R H I L R F N 400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG 1260
401 R P F L V V I F S T S T Q S V L F L G K 420

1261 GTCGTCGACCCACGAAACCATAG 1284
421 V V D P T K P * 428

Figure 45A

1	ATGCATCTTATCGACTACCTGCTCCTCCTGCTGGTTGGACTACTGGCCCTTTCTCATGGC	60
1	M H L I D Y L L L L L V G L L A L S H G	20
61	CAGCTGCACGTTGAGCATGATGGTGAGAGTTGCAGTAACAGCTCCCACCAGCAGATTCTG	120
21	Q L H V E H D G E S C S N S S H Q Q I L	40
121	GAGACAGGTGAGGGCTCCCCAGCCTCAAGATAGCCCCTGCCAATGCTGACTTTGCCTTC	180
41	E T G E G S P S L K I A P A N A D F A F	60
181	CGCTTCTACTACCTGATCGCTTCGGAGACCCCGGGGAAGAACATCTTTTCTCCCCGCTG	240
61	R F Y Y L I A S E T P G K N I F F S P L	80
241	AGCATCTCGGCGGCCTACGCCATGCTTTCCCTGGGGGCTGCTCACACAGCCGCAGCCAG	300
81	S I S A A Y A M L S L G A C S H S R S Q	100
301	ATCCTTGAGGGCCTGGGCTTCAACCTCACCGAGCTGTCTGAGTCCGATGTCCATAGGGGC	360
101	I L E G L G F N L T E L S E S D V H R G	120
361	TTCCAGCACCTCCTGCACACTCTCAACCTCCCCGGCCATGGGCTGGAAACATGCGTGGGC	420
121	F Q H L L H T L N L P G H G L E T C V G	140
421	AGTGCTCTGTTCCCTGAGCCACAACCTGAAGTTCCTTGCAAAATTCCTGAATGACACCATG	480
141	S A L F L S H N L K F L A K F L N D T M	160
481	GCCGTCTATGAGGCTAAACTCTTCCACACCAACTTCTACGACACTGTGGGCACAATCCAG	540
161	A V Y E A K L F H T N F Y D T V G T I Q	180
541	CTTATCAACGACCACGTCAAGAAGGAAACTCGAGGGAAGATTGTGGATTGGTTCAGTGAG	600
181	L I N D H V K K E T R G K I V D L V S E	200
601	CTCAAGAAGGACGTCTTGATGGTGCTGGTGAATTACATTTACTTCAAAGCCCTGTGGGAG	660
201	L K K D V L M V L V N Y I Y F K A L W E	220
661	AAACCATTCAATTCCTCAAGGACCACTCCCAAAGACTTCTATGTTGATGAGAACACAACA	720
221	K P F I S S R T T P K D F Y V D E N T T	240
721	GTCCGGGTGCCCCATGATGCTGCAGGACCAGGAGCATCACTGGTATCTTCATGACAGATAC	780
241	V R V P M M L Q D Q E H H W Y L H D R Y	260
781	TTGCCCTGCTCGGTGCTACGGATGGATTACAAAGGAGACGCAACCGTGTTTTTCATTCTC	840
261	L P C S V L R M D Y K G D A T V F F I L	280

Figure 45B

841 CCTAACCAAGGCAAATGAGGGAGATTGAAGAGGTTCTGACTCCAGAGATGCTAATGAGG 900
281 P N Q G K M R E I E E V L T P E M L M R 300

901 TGGAACAACCTTGTTCGGAAGAGGAATTTTACAAGAAGCTAGAGTTGCATCTTCCAAG 960
301 W N N L L R K R N F Y K K L E L H L P K 320

961 TTCTCCATTTCTGGCTCCTATGTATTAGATCAGATTTTGCCCAGGCTGGGCTTCACGGAT 1020
321 F S I S G S Y V L D Q I L P R L G F T D 340

1021 CTGTTCTCCAAGTGGGCTGACTTATCCGGCATCACCAAACAGCAAAAACTGGAGGCATCC 1080
341 L F S K W A D L S G I T K Q Q K L E A S 360

1081 AAAAGTTTCCACAAGGCCACCTTGGACGTGGATGAGGCTGGCACCGAGGCTGCAGCAGCC 1140
361 K S F H K A T L D V D E A G T E A A A A 380

1141 ACCACGTTCGCGATCAAATTCTTCTCTGCCCAGACCAATCGCCACATCCTGCGATTCAAC 1200
381 T T F A I K F F S A Q T N R H I L R F N 400

1201 CGGCCCTTCCTTGTGGTGATCTTTTCCACCAGCACCCAGAGTGTCTCTTTCTGGGCAAG 1260
401 R P F L V V I F S T S T Q S V L F L G K 420

1261 GTCGTCGACCCACGAAACCATAG 1284
421 V V D P T K P * 428

Figure 46A

1 CACCCTATCC TACTACTACTA GGAACCTTGCA CAGTCCGCCT CGGGCAGCCC AAAGCTCCTC 60
 61 TGCCCAACCCT GGCTCCCAA ACCCTCCAAA ACAAAGACC AGAAAAGCAC TCTCCACCCA 120
 121 GCAGCCAAAC GCCTCCTTCT TGACGCCAGC CCCACCCCTC TGTCTGCTCG AGCCAGGAA 180
 181 AGGCCTGAAG GAACAGGCCG GGAAGGAGC CCTCCCTCTC TCCCTTGCTC CTCCATCCAC 240
 241 CCAGCGCCCG CATCTGGAGA CCCTATGGCC CGGGCTCACT GGGGCTGCTG CCCCTGGCTG 300
 1 M A R A H W G C C P W L 12
 301 GTCCTCCTCT GTGCTTGTGC CTGGGGCCAC ACAAAGCCAC TGGACCTTGG AGGGCAGGAT 360
 13 V L L C A C A W G H T K P L D L G G Q D 32
 361 GTGAGAAATT GTTCCACCAA CCCCCCTTAC CTTCAGTTA CTGTGGTCAA TACCACAATG 420
 33 V R N C S T N P P Y L P V T V V N T T M 52
 421 TCACTCACAG CCCTCCGCCA GCAGATGCAG ACCCAGAATC TCTCAGCCTA CATCATCCCA 480
 53 S L T A L R Q Q M Q T Q N L S A Y I I P 72
 481 GGCACAGATG CTCACATGAA CGAGTACATC GGCCAACATG ACGAGAGGCG TGCCTGGATT 540
 73 G T D A H M N E Y I G Q H D E R R A W I 92
 541 ACAGGCTTTA CAGGGTCTGC AGGAACTGCA GTGGTGAATA TGAAGAAAGC AGCTGTCTGG 600
 93 T G F T G S A G T A V V T M K K A A V W 112
 601 ACCGACAGTC GCTACTGGAC TCAGGCTGAG CGGCAAATGG ACTGTAATTG GGAGCTCCAT 660
 113 T D S R Y W T Q A E R Q M D C N W E L H 132
 661 AAGGAAGTTG GCACCACTCC TATTGTCACC TGGCTCCTCA CCGAGATTCC NGCTGGAGGG 720
 133 K E V G T T P I V T W L L T E I P A G G 152
 721 CGTGTGGGTT TTGACCCCTT CCTCTTGCTC ATTGACACCT GGGAGAGTTA TGATCTGGCC 780
 153 R V G F D P F L L S I D T W E S Y D L A 172
 781 CTCCAAGGCT CTAACAGACA GCTGGTGTCC ATCACAACCA ATCTTGTTGA CCTGGTATGG 840
 173 L Q G S N R Q L V S I T T N L V D L V W 192
 841 GGATCAGAGA GGCCACCGGT TCCAAATCAA CCCATTTATG CCCTGCAGGA GGCATTCACA 900
 193 G S E R P P V P N Q P I Y A L Q E A F T 212
 901 GGGAGCACTT GGCAGGAGAA AGTATCTGGC GTCCGAAGCC AGATGCAGAA GCATCAAAAG 960
 213 G S T W Q E K V S G V R S Q M Q K H Q K 232

Figure 46B

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961 GTCCCGACTG CCGTCCTTCT GTCGGCGCTT GAGGAGACGG CCTGGCTCTT CAACCTTCGA 1020
233 V P T A V L L S A L E E T A W L F N L R 252

1021 GCCAGTGACA TCCCCTATAA CCCCTTCTTC TATTCCTACA CGCTGCTCAC AGACTCTTCT 1080
253 A S D I P Y N P F F Y S Y T L L T D S S 272

1081 ATTAGGTTGT TTGCAAACAA GAGTCGCTTT AGCTCCGAAA CCTTGAGCTA TCTGAACTCC 1140
273 I R L F A N K S R F S S E T L S Y L N S 292

1141 AGTTGCACAG GCCCCATGTG TGTGCAAATC GAGGATTACA GCCAAGTTCTG TGACAGCATC 1200
293 S C T G P M C V Q I E D Y S Q V R D S I 312

1201 CAGGCCTACT CATTGGGAGA TGTGAGGATC TGGATTGGGA CCAGCTATAC CATGTATGGG 1260
313 Q A Y S L G D V R I W I G T S Y T M Y G 332

1261 ATCTATGAAA TGATACCAAG GGAGAAACTC GTGACAGACA CCTACTCCCC AGTGATGATG 1320
333 I Y E M I P R E K L V T D T Y S P V M M 352

1321 ACCAAGGCAG TGAAGAACAG CAAGGAGCAG GCCCTCCTCA AGGCCAGCCA CGTGCGGGAC 1380
353 T K A V K N S K E Q A L L K A S H V R D 372

1381 GCTGTGGCTG TGATCCGGTA CTTGGTCTGG CTGGAGAAGA ACGTGCCCAA AGGCACAGTG 1440
373 A V A V I R Y L V W L E K N V P K G T V 392

1441 GATGAGTTTT CGGGGGCAGA GATCGTGGAC AAGTTCCGAG GAGAAGAACA GTTCTCTCTC 1500
393 D E F S G A E I V D K F R G E E Q F S S 412

1501 GGACCCAGTT TTGAAACCAT CTCTGCTAGT GGTTTGAATG CTGCCCTGGC CCACTACAGC 1560
413 G P S F E T I S A S G L N A A L A H Y S 432

1561 CCGACCAAGG AGCTGAACCG CAAGCTGTCC TCAGATGAGA TGTACCTGCT GGACTCTGGG 1620
433 P T K E L N R K L S S D E M Y L L D S G 452

1621 GGGCAGTACT GGGACGGGAC CACAGACATC ACCAGAACAG TCCACTGGGG CACCCCTCT 1680
453 G Q Y W D G T T D I T R T V H W G T P S 472

1681 GCCTTTCAGA AGGAGGCATA TACCCGTGTG CTGATAGGAA ATATTGACCT GTCCAGGCTC 1740
473 A F Q K E A Y T R V L I G N I D L S R L 492

1741 ATCTTTCCCG CTGCTACATC AGGGCGAATG GTGGAGGCCT TTGCCCGCAG AGCCTTGTGG 1800
493 I F P A A T S G R M V E A F A R R A L W 512

1801 GATGCTGGTC TCAATTATGG TCATGGGACA GGCCACGGCA TTGGCAACTT CCTGTGTGTG 1860
513 D A G L N Y G H G T G H G I G N F L C V 532

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Figure 46C

1861 CATGAGTGGC CAGTGGGATT CCAGTCCAAC AACATCGCTA TGGCCAAGGG CATGTTCACT 1920
 533 H E W P V G F Q S N N I A M A K G M F T 552

1921 TCCATTGAAC CTGGTTACTA TAAGGATGGA GAATTTGGGA TCCGTCTCGA AGATGTGGCT 1980
 553 S I E P G Y Y K D G E F G I R L E D V A 572

1981 CTCGTGGTAG AAGCAAAGAC CAAGTACCCA GGGGAGCTAC CTGACCTTGT GGTATCATT 2040
 573 L V V E A K T K Y P G E L P D L V V S F 592

2041 GTGCCCTATG ACCGGAACCT CATCGATGTC AGCCTGCTGT CTCCNGAGCA TCTCCAGTAC 2100
 593 V P Y D R N L I D V S L L S P E H L Q Y 612

2101 CTGAATCGCT ACTACCAGAC CATCCGGGAG AAGGTGGGTC CAGAGCTGCA GAGGCGCCAG 2160
 613 L N R Y Y Q T I R E K V G P E L Q R R Q 632

2161 CTACTAGAGG AGTTCGAGTG GCTTCAACAG CACACAGAGC CCCTGGCCGC CAGGGCCCCA 2220
 633 L L E E F E W L Q Q H T E P L A A R A P 652

2221 GACACCGCCT CCTGGGCCTC TGTGTTAGTG GTCTCCACCC TTGCCATCCT TGGCTGGAGT 2280
 653 D T A S W A S V L V V S T L A I L G W S 672

2281 GTCTAGAGGC TCCAGACTCT CCTGTTAACC CTCCATCTAG ATGGGGGGCT CCCTTGCTTA 2340
 673 V * 673

2341 GCTCCCCTCA CCCTGCACTG AACATACCCC AAGAGCCCCT GCTGGCCCAT TGCCTAGAAA 2400

2401 CCTTTGCATT CATCCTCCTT CTCCAAGACC TATGGAGAAG GTCCCAGGCC CCAGGAAACA 2460

2461 CAGGGCTTCT TGGCCCCAGA TGGCACCTCC CTGCACCCCG GGGTTGTATA CCACACCCTG 2520

2521 GGCCCCTAAT CCCAGGCCCC GAAATAGGAA AGCCAGCTAG TCTCTTCTCT TCTGTGATCT 2580

2581 CAGTAGGCCT AACCTATAAC CTAACACAGA CTGCTACAGC TGCTCCCCTC CCGCCAAACA 2640

2641 AAGCCCCAAG AAAACAATGC CCCTACCACC CAAGGGTGCC ATGGTCCCGG GAAAACCCAA 2700

2701 CCTGTCACCG CGTGTGGGC GTAACCAGAA CTGTTCCCCC CCACCAGGGC TTAAAAATCG 2760

2761 CCCCCACTTT TTAACCATCG TCCATTAACC ACCTGGTGGG CATAGCCAGA GCTGTTCGAA 2820

2821 CCCAGCCAGG GATGAAAAAT CAACCCCGA CATGGAACCC ATGATTCTTA AACCCGGGGT 2880

2881 AGGTTCCATG CCAAGTAACA GCAGAGGGAG TTAAGCCATA GGAATTTGGC TGTGGAGTAA 2940

Figure 46D

2941 GAGGGAATGC GGTGAGGCAG TGTGGAATAT GACCCTACCA GAGGTGGAG AACAAACTTG 3000
3001 GGCAGCCGGA ACCCGTCACT ATTTTAGATT CCTGGCATTG GAGGAGCCCT TTGAACTTTC 3060
3061 CAAAGTGCAG CCACAGCTAC AATGCTGTTA AATCCTCCCA CATTTCTTGG ATGCCCCCTC 3120
3121 ACCTTGTGTG GACAGTGTCT GGTTCCTCCA TTTTACAGAC AGGAAACTG AGCTTCAGAC 3180
3181 AGGGGGTGGG CTTGCCTAA GGACACACAA ATTTGGTTGG GAGTTGATGG GGCCAGATGA 3240
3241 GCCAGCATTG CAGCTGTTTC ACCCTTCAGC AACATGCAGA GTCCCTGAGC CCACCTCCCA 3300
3301 GCCCTCTCCT CATTCTCTGA ACCCACTGTG GTGAGAAGAA TTTGCTCCGG CCAAATTGGC 3360
3361 CGTTAGCCAC CTGGGTCCAC ATCCTGCTAA GACGTTTAAA ACAGCCTAAC AAAGACACTT 3420
3421 GCCTGTGG 3428

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